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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/081,864

DATE: 06/28/2002
TIME: 10:33:12

Input Set : D:\seqlist.txt
Output Set: N:\CRF3\06282002\J081864.raw

4 <110> APPLICANT: Lukyanov, Sergey
 5 Lukyanov, Konstantin
 6 Yanushevich, Yuriy
 7 Savistky, Alexandr
 8 Fradkov, Arcady
 10 <120> TITLE OF INVENTION: Non Aggregating Fluorescent Proteins and
 11 Methods for Using the Same
 14 <130> FILE REFERENCE: CLON-067
 16 <140> CURRENT APPLICATION NUMBER: 10/081,864
 C--> 17 <141> CURRENT FILING DATE: 2002-06-19
 19 <150> PRIOR APPLICATION NUMBER: 10/006,922
 20 <151> PRIOR FILING DATE: 2001-12-04
 22 <150> PRIOR APPLICATION NUMBER: 60/270,983
 23 <151> PRIOR FILING DATE: 2001-02-21
 25 <160> NUMBER OF SEQ ID NOS: 30
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 37 acgcagacct cgactttaa agtcaccatg gccaacggtg ggcccttgc attctcctt 180
 38 gacatactat ctacagtgtt caagtatgaa aatcgatgct ttactgcgtt tcctaccagt 240
 39 atgcccgcact atttcaaaca agcatttcct gacggaatgt catatgaaag gactttacc 300
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 41 gagcacaat ccacgttca tgagtgAAC tttcctgctg atggacctgt gatggcgaag 420
 42 atgacaactg gttgggaccc atctttgag aaaatgactg tctgcgttgg aatattgaag 480
 43 ggtgatgtca ccgcgttcc catgctgcaa ggaggtggca attacagatg ccaattccac 540
 44 acttcttaca agacaaaaaa accggtgacg atgcccacaa accatgcggg ggaacatcgc 600
 45 attgcgagga ccgacattga caaagggtggc aacagtgttc agctgacggg gcacgctgtt 660
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 50 <212> TYPE: PRT
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 57 20 25 30
 58 Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val

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 60 Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
 61 50 55 60
 62 Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
 63 65 70 75 80
 64 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 65 85 90 95
 66 Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
 67 100 105 110
 68 Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
 69 115 120 125
 70 Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Met Thr Thr Gly
 71 130 135 140
 72 Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys
 73 145 150 155 160
 74 Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Asn Tyr Arg
 75 165 170 175
 76 Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro
 77 180 185 190
 78 Pro Asn His Ala Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys
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 94 aaacaggcta ttaatctgtg tttgttcgaa ggtggaccat tgccatttgc cgaagacata 180
 95 ttgtcagctg ctttatgtt cggaaaacagg gttttcactg aatatcctca agacatagct 240
 96 gactattca agaactctgtc ttctgtcggt tatacatggg acaggtctt tctctttgag 300
 97 gatggagcag tttgcataatg taatgcagat ataacagtga gtgttgaaga aaactgcgt 360
 98 tatcatgagt ccaaattttt tggagtgaat ttccctgtc atggacctgt gatgaaaaag 420
 99 atgacagata actgggagcc atcctgcgag aagatcatac cagttaccaa gcaggggata 480
 100 ttgaaagggg atgtctccat gtacccctt ctgaaggatg gtggcggtt acgggtccaa 540
 101 ttgcacacag ttacaaagc aaagtctgtc ccaagaaaga tgccggactg gcacttcatc 600
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 106 <211> LENGTH: 231
 107 <212> TYPE: PRT
 108 <213> ORGANISM: Zoanthus sp.
 110 <400> SEQUENCE: 4
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115 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val
116 35 40 45
117 Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala
118 50 55 60
119 Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala
120 65 70 75 80
121 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser
122 85 90 95
123 Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr
124 100 105 110
125 Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly
126 115 120 125
127 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn
128 130 135 140
129 Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile
130 145 150 155 160
131 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg
132 165 170 175
133 Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg
134 180 185 190
135 Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp
136 195 200 205
137 Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile
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139 Ala Ser Gly Ser Ala Leu Pro
140 225 230
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150 catggctcat tcaaagcacg gtctaaaaga agaaatgaca atgaaatacc acatgaaagg 120
151 gtgcgtcaac ggcataaaat ttgtgatcac gggcgaaggc attggatatc cgttcaaagg 180
152 gaaacagact attaatctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240
153 attgtcagct ggcttaagt acggagacag gatttcaact gaatatcctc aagacatagt 300
154 agactattc aagaactcgt gtccctgctgg atatacatgg ggcagggtctt ttctcttga 360
155 ggatggagca gtctgcataat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat 420
156 ttatcataaag agcatattta atggaatgaa tttccctgct gatggacctg tgataaaaaa 480
157 gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcagggat 540
158 actgaaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggcgtt accgggtgcca 600
159 gttcgacaca gtttacaaag caaagtctgt gccaagtaag atgcccggagt ggcacttcat 660
160 ccagcataaag ctcctccgtg aagaccgcag cgtatgtaag aatcagaagt ggcagctgac 720
161 agagcatgtt attgcattcc ctctgcctt ggcctgataa gaatgttagtt ccaacatttt 780
162 aatgcatgtt cttgtcaatt attctgataa aatgttagtt gagttgaaaaa cagacaagta 840
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173 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu
174 20 25 30
175 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val
176 35 40 45
177 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly
178 50 55 60
179 Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val
180 65 70 75 80
181 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Ser Phe
182 85 90 95
183 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
184 100 105 110
185 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Met
186 115 120 125
187 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
188 130 135 140
189 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
190 145 150 155 160
191 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
192 165 170 175
193 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
194 180 185 190
195 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
196 195 200 205
197 Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
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200 225 230
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204 <211> LENGTH: 678
205 <212> TYPE: DNA
206 <213> ORGANISM: Discosoma sp
208 <400> SEQUENCE: 7
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211 cacaacacccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180
212 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcacccccc cgacatcccc 240
213 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgtat gaacttcgag 300
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216 atgggctggg aggcctccac cgagcgcctg taccggcgacggcgtgtat gaaggcggag 480
217 atccacaagg ccctgaagct gaaggacgcg ggcactacc tggtgaggat caagtccatc 540
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224 <212> TYPE: PRT
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227 <400> SEQUENCE: 8
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229 1 5 10 15
230 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
231 20 25 30
232 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
233 35 40 45
234 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
235 50 55 60
236 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
237 65 70 75 80
238 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
239 85 90 95
240 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
241 100 105 110
242 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
243 115 120 125
244 Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
245 130 135 140
246 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
247 145 150 155 160
248 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
249 165 170 175
250 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
251 180 185 190
252 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
253 195 200 205
254 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
255 210 215 220
256 Leu
257 225
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 696
262 <212> TYPE: DNA
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265 <400> SEQUENCE: 9
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268 atgaagatag aggtcatcga aggaggtcca ttgccatttgc cttccacat tttgtcaacg 180
269 agttgtatgt acggtagtaa ggccttcattc aagtatgtgt caggaattcc tgactacttc 240
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271 tttcttacag ctcatcagga cacaaggcata gatggagatt gcctcggttcaaggtcaag 360
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VERIFICATION SUMMARY DATE: 06/28/2002
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